

SEQUENCE LISTING

<110> Allan, Bernard
Lavan, Brian
Moodie, Shonna
Waters, Steve
Wong, Chi-Wai
Metabolex, Inc.

<120> Methods of Diagnosing & Treating Diabetes and Insulin
Resistance

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<140> US 10/516,803
<141> 2004-12-02

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<151> 2002-06-04

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<150> WO PCT/US03/17941
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<170> PatentIn Ver. 2.1

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His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
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Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
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Leu Pro Tyr Val Lys Lys Thr Gly Met Phe Ser Ile Arg Leu Pro Asn
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Lys Tyr Asn Val Ser Phe Asp Tyr Tyr Tyr Phe Leu Leu Ile Thr Met
245 250 255
Ala Ser Tyr Ile Pro Leu Phe Pro Gln Leu Tyr Phe His Met Leu Arg
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 (PTPLA) cDNA

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 35 40 45

Ser Asp Glu Lys Glu Ala Ala Gly Lys Arg Arg Arg Leu Gly Leu Leu
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Ala Thr Ala Trp Leu Thr Phe Tyr Asn Ile Ala Met Thr Ala Gly Trp
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Leu Val Leu Ala Ile Ala Met Val Arg Phe Tyr Met Glu Lys Gly Thr
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His Arg Gly Leu Tyr Lys Ser Ile Gln Lys Thr Leu Lys Phe Phe Gln
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Thr Phe Ala Leu Leu Glu Val Val His Cys Leu Ile Gly Ile Val Pro
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 Thr Ser Val Leu Val Thr Gly Val Gln Val Ser Ser Arg Ile Phe Met
 130 135 140
 Val Trp Leu Ile Thr His Ser Ile Lys Pro Ile Gln Asn Glu Glu Ser
 145 150 155 160
 Val Val Leu Phe Leu Val Ser Trp Thr Val Thr Glu Ile Thr Arg Tyr
 165 170 175
 Ser Phe Tyr Thr Phe Ser Leu Leu Asp His Leu Pro His Phe Ile Lys
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 Trp Ala Arg Tyr Asn Leu Phe Ile Ile Leu Tyr Pro Val Gly Val Ala
 195 200 205
 Gly Glu Leu Leu Thr Ile Tyr Ala Ala Leu Pro Tyr Val Lys Lys Ser
 210 215 220
 Gly Met Phe Ser Val Arg Leu Pro Asn Lys Tyr Asn Val Ser Phe Asp
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 Tyr Tyr Tyr Phe Leu Leu Ile Thr Met Ala Ser Tyr Ile Pro Leu Phe
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 Gly Glu Val Ile Ala Glu Lys Asp Asp
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 cDNA

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| | | | | | | |
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| tgtctccacc | tgatgggtca | tcatacataa | aatgaggaga | gctggcacga | tggtgtccgg | 1920 |
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| tgtggcaacc | ccaccattca | ccctggacag | tgtgcccct | catgtgcaga | tgactttgtg | 2040 |
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Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
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Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
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Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
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Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
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Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
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Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
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| | | | | | | | | | | | | | | | | |
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| Leu | Ser | Ala | Leu | Lys | Arg | Ile | Glu | Glu | Glu | Lys | Pro | Asp | Cys | Ser | Lys | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| Ala | Arg | Cys | Glu | Val | Gln | Phe | Ser | Pro | Arg | Cys | Pro | Glu | Asp | Ser | Val | |
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| Leu | Ile | Glu | Gly | Tyr | Ala | Pro | Pro | Gly | Glu | Cys | Cys | Pro | Leu | Pro | Ser | |
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| Arg | Cys | Val | Cys | Asn | Pro | Ala | Gly | Cys | Leu | Arg | Lys | Val | Cys | Gln | Pro | |
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| Gly | Asn | Leu | Asn | Ile | Leu | Val | Ser | Lys | Ala | Ser | Gly | Lys | Pro | Gly | Glu | |
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| Cys | Cys | Asp | Leu | Tyr | Glu | Cys | Lys | Pro | Val | Phe | Gly | Val | Asp | Cys | Arg | |
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| Tyr | Glu | Thr | Gln | Val | Arg | Leu | Thr | Ala | Asp | Gly | Cys | Cys | Thr | Leu | Pro | |
| | | 275 | | | | | 280 | | | | | | 285 | | | |
| Thr | Arg | Cys | Glu | Cys | Leu | Ser | Gly | Leu | Cys | Gly | Phe | Pro | Val | Cys | Glu | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Val | Gly | Ser | Thr | Pro | Arg | Ile | Val | Ser | Arg | Gly | Asp | Gly | Thr | Pro | Gly | |
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| Lys | Cys | Cys | Asp | Val | Phe | Glu | Cys | Val | Asn | Asp | Thr | Lys | Pro | Ala | Cys | |
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| Asn | Cys | Arg | Phe | Cys | Arg | Cys | Gln | Gly | Gly | Val | Ala | Ile | Cys | Phe | Thr | |
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| Ala | Gln | Cys | Gly | Glu | Ile | Asn | Cys | Glu | Arg | Tyr | Tyr | Val | Pro | Glu | Gly | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Glu | Cys | Cys | Pro | Val | Cys | Glu | Asp | Pro | Val | Tyr | Pro | Phe | Asn | Asn | Pro | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ala | Gly | Cys | Tyr | Ala | Asn | Gly | Leu | Ile | Leu | Ala | His | Gly | Asp | Arg | Trp | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Arg | Glu | Asp | Asp | Cys | Thr | Phe | Cys | Gln | Cys | Val | Asn | Gly | Glu | Arg | His | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Cys | Val | Ala | Thr | Val | Cys | Gly | Gln | Thr | Cys | Thr | Asn | Pro | Val | Lys | Val | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| Pro | Gly | Glu | Cys | Cys | Pro | Val | Cys | Glu | Glu | Pro | Thr | Ile | Ile | Thr | Val | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Pro | Ala | Cys | Gly | Glu | Leu | Ser | Asn | Cys | Thr | Leu | Thr | Gly | Lys | 465 | 470 | 475 | 480 |
| Asp | Cys | Ile | Asn | Gly | Phe | Lys | Arg | Asp | His | Asn | Gly | Cys | Arg | Thr | Cys | 485 | 490 | 495 | |
| Gln | Cys | Ile | Asn | Thr | Glu | Glu | Leu | Cys | Ser | Glu | Arg | Lys | Gln | Gly | Cys | 500 | 505 | 510 | |
| Thr | Leu | Asn | Cys | Pro | Phe | Gly | Phe | Leu | Thr | Asp | Ala | Gln | Asn | Cys | Glu | 515 | 520 | 525 | |
| Ile | Cys | Glu | Cys | Arg | Pro | Arg | Pro | Lys | Lys | Cys | Arg | Pro | Ile | Ile | Cys | 530 | 535 | 540 | |
| Asp | Lys | Tyr | Cys | Pro | Leu | Gly | Leu | Leu | Lys | Asn | Lys | His | Gly | Cys | Asp | 545 | 550 | 555 | 560 |
| Ile | Cys | Arg | Cys | Lys | Lys | Cys | Pro | Glu | Leu | Ser | Cys | Ser | Lys | Ile | Cys | 565 | 570 | 575 | |
| Pro | Leu | Gly | Phe | Gln | Gln | Asp | Ser | His | Gly | Cys | Leu | Ile | Cys | Lys | Cys | 580 | 585 | 590 | |
| Arg | Glu | Ala | Ser | Ala | Ser | Ala | Gly | Pro | Pro | Ile | Leu | Ser | Gly | Thr | Cys | 595 | 600 | 605 | |
| Leu | Thr | Val | Asp | Gly | His | His | His | Lys | Asn | Glu | Glu | Ser | Trp | His | Asp | 610 | 615 | 620 | |
| Gly | Cys | Arg | Glu | Cys | Tyr | Cys | Leu | Asn | Gly | Arg | Glu | Met | Cys | Ala | Leu | 625 | 630 | 635 | 640 |
| Ile | Thr | Cys | Pro | Val | Pro | Ala | Cys | Gly | Asn | Pro | Thr | Ile | His | Pro | Gly | 645 | 650 | 655 | |
| Gln | Cys | Cys | Pro | Ser | Cys | Ala | Asp | Asp | Phe | Val | Val | Gln | Lys | Pro | Glu | 660 | 665 | 670 | |
| Leu | Ser | Thr | Pro | Ser | Ile | Cys | His | Ala | Pro | Gly | Gly | Glu | Tyr | Phe | Val | 675 | 680 | 685 | |
| Glu | Gly | Glu | Thr | Trp | Asn | Ile | Asp | Ser | Cys | Thr | Gln | Cys | Thr | Cys | His | 690 | 695 | 700 | |
| Ser | Gly | Arg | Val | Leu | Cys | Glu | Thr | Glu | Val | Cys | Pro | Pro | Leu | Leu | Cys | 705 | 710 | 715 | 720 |
| Gln | Asn | Pro | Ser | Arg | Thr | Gln | Asp | Ser | Cys | Cys | Pro | Gln | Cys | Thr | Asp | 725 | 730 | 735 | |
| Gln | Pro | Phe | Arg | Pro | Ser | Leu | Ser | Arg | Asn | Asn | Ser | Val | Pro | Asn | Tyr | 740 | 745 | 750 | |
| Cys | Lys | Asn | Asp | Glu | Gly | Asp | Ile | Phe | Leu | Ala | Ala | Glu | Ser | Trp | Lys | 755 | 760 | 765 | |
| Pro | Asp | Val | Cys | Thr | Ser | Cys | Ile | Cys | Ile | Asp | Ser | Val | Ile | Ser | Cys | 770 | 775 | 780 | |

Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg Pro Val Leu Arg
785 790 795 800
Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr Ile Pro Lys Lys
805 810 815
Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp Glu Glu Arg Trp
820 825 830
Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln Gly Gln Thr Leu
835 840 845
Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val Glu Pro Ile Asn
850 855 860
Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met Tyr Val Pro Glu
865 870 875 880
Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg Gly Glu Val Asp
885 890 895
Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn Asp Ile Val His
900 905 910
Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr Arg Asp Asn Arg
915 920 925
Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val
930 935 940
Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile
945 950 955 960
Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp Tyr Arg Thr Pro
965 970 975
Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser Val Asp Cys Lys
980 985 990
Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile
995 1000 1005
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Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val
1025 1030 1035

<210> 13

<211> 4012

<212> DNA

<213> Mus musculus

<220>

<223> mouse cysteine-rich repeat-containing protein,
cysteine-rich motorneuron 1 (CRIM1) partial cDNA

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<220>
<221> CDS
<222> (1)..(3087)
<223> CRIM1

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<220>
<221> modified_base
<222> (3515)
<223> n = g, a, c or t

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<210> 14

<211> 1028

<212> PRT

<213> Mus musculus

<220>

<223> mouse cysteine-rich repeat-containing protein,
cysteine-rich motorneuron 1 (CRIM1), partial

<400> 14

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Leu Ala Gly Cys Gly His Leu Ser Val Ser Leu Leu Gly Leu Leu Leu
  1              5              10              15

```

```

Leu Leu Ala Arg Ser Gly Thr Arg Ala Leu Val Cys Leu Pro Cys Asp
      20              25              30

```

```

Glu Ser Lys Cys Glu Glu Pro Arg Ser Cys Pro Gly Ser Ile Val Gln
      35              40              45

```

```

Gly Val Cys Gly Cys Cys Tyr Met Cys Ala Arg Gln Arg Asn Glu Ser
      50              55              60

```

```

Cys Gly Gly Ala Tyr Gly Leu His Gly Ala Cys Asp Arg Gly Leu Arg
      65              70              75              80

```

```

Cys Val Ile Arg Pro Pro Leu Asn Gly Asp Ser Ile Thr Glu Tyr Glu
      85              90              95

```

```

Val Gly Val Cys Glu Asp Glu Asp Trp Asp Asp Asp Gln Leu Ile Gly
      100             105             110

```

```

Phe Glu Pro Cys Asn Glu Asn Leu Ile Ser Gly Cys Asn Ile Ile Asn
      115             120             125

```

```

Gly Lys Cys Glu Cys Gly Thr Ile Arg Thr Cys Asn Asn Pro Phe Glu
      130             135             140

```

```

Phe Pro Arg Lys Asp Met Cys Leu Ser Ala Leu Lys Arg Ile Glu Glu
      145             150             155             160

```

```

Glu Lys Pro Asp Cys Ser Lys Ala Arg Cys Glu Val Arg Phe Ser Pro
      165             170             175

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Arg Cys Pro Glu Asp Ser Ile Leu Ile Glu Gly Tyr Ala Pro Pro Gly
 180 185 190
 Glu Cys Cys Pro Leu Pro Ser Arg Cys Val Cys Asp Pro Ala Gly Cys
 195 200 205
 Leu Arg Lys Val Cys Gln Pro Gly Tyr Leu Asn Ile Leu Val Ser Lys
 210 215 220
 Ala Ser Gly Lys Pro Gly Glu Cys Cys Asp Leu Tyr Glu Cys Lys Pro
 225 230 235 240
 Val Phe Ser Val Asp Cys Ser Thr Val Glu Cys Pro Pro Val Gln Gln
 245 250 255
 Ala Val Cys Pro Leu Asp Ser Tyr Glu Thr Gln Val Arg Leu Thr Ala
 260 265 270
 Asp Gly Cys Cys Thr Leu Pro Ala Arg Cys Glu Cys Leu Ser Gly Leu
 275 280 285
 Cys Gly Phe Pro Val Cys Glu Val Gly Ser Thr Pro Arg Ile Val Ser
 290 295 300
 Arg Gly Asp Gly Thr Pro Gly Lys Cys Cys Asp Val Phe Glu Cys Val
 305 310 315 320
 Asn Glu Thr Lys Pro Ala Cys Val Phe Asn Ser Val Glu Tyr Tyr Asp
 325 330 335
 Gly Asp Met Phe Arg Met Asp Asn Cys Arg Phe Cys Arg Cys Gln Gly
 340 345 350
 Gly Val Ser Ile Cys Phe Thr Ala Gln Cys Gly Glu Leu Asn Cys Glu
 355 360 365
 Arg Tyr Tyr Val Pro Glu Gly Glu Cys Cys Pro Val Cys Glu Asp Pro
 370 375 380
 Ile Tyr Pro Leu Asn Asn Pro Ala Gly Cys Tyr Ala Asn Gly Gln Ile
 385 390 395 400
 Arg Ala His Gly Asp Arg Trp Arg Glu Asp Asp Cys Thr Phe Cys Gln
 405 410 415
 Cys Ile Asn Gly Glu Pro His Cys Val Ala Thr Ala Cys Gly Gln Ser
 420 425 430
 Cys Met His Pro Val Lys Val Pro Gly Glu Cys Cys Pro Val Cys Glu
 435 440 445
 Glu Pro Thr Tyr Ile Thr Ile Asp Pro Pro Ala Cys Gly Glu Leu Ser
 450 455 460
 Asn Cys Ser Leu Lys Glu Lys Asp Cys Val Tyr Gly Phe Lys Leu Asp
 465 470 475 480
 His Asn Gly Cys Arg Thr Cys Gln Cys Lys Ile Arg Glu Glu Leu Cys
 485 490 495

Leu Gly Leu Lys Arg Ala Cys Thr Leu Asp Cys Pro Phe Gly Phe Leu
 500 505 510
 Thr Asp Val His Asn Cys Glu Leu Cys Gln Cys Arg Pro Arg Pro Lys
 515 520 525
 Lys Cys Arg Pro Thr Met Cys Asp Lys Phe Cys Pro Leu Gly Phe Leu
 530 535 540
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 545 550 555 560
 Leu Pro Cys Ser Lys Ile Cys Pro Leu Gly Phe Gln Gln Asp Ser His
 565 570 575
 Gly Cys Leu Ile Cys Lys Cys Arg Glu Val Pro Pro Ser Ala Gly Pro
 580 585 590
 Pro Val Leu Ser Gly Thr Cys Leu Ser Met Asp Gly His His His Lys
 595 600 605
 Asn Glu Glu Ser Trp His Asp Gly Cys Arg Glu Cys Tyr Cys His Asn
 610 615 620
 Gly Lys Glu Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly
 625 630 635 640
 Asn Pro Thr Ile Arg Ser Gly Gln Cys Cys Pro Ser Cys Thr Asp Asp
 645 650 655
 Phe Val Val Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala
 660 665 670
 Pro Gly Gly Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser
 675 680 685
 Cys Thr Gln Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu
 690 695 700
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 705 710 715 720
 Cys Cys Pro Gln Cys Thr Asp Asp Pro Pro Gln Pro Ser Thr Ser His
 725 730 735
 Asn Glu Ser Val Pro Ser Tyr Cys Arg Asn Asp Glu Gly Asp Ile Phe
 740 745 750
 Leu Ala Ala Glu Ser Trp Lys Pro Asp Ala Cys Thr Ser Cys Val Cys
 755 760 765
 Val Asp Ser Ala Ile Ser Cys Tyr Ser Glu Ser Cys Pro Ser Val Ala
 770 775 780
 Cys Glu Arg Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Leu
 785 790 795 800
 Glu Asp Thr Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Thr
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Tyr Ala Asp Glu Glu Arg Trp Asp Ile Asp Ser Cys Thr His Cys Tyr
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 Pro Cys Ala Glu Pro Ile Lys Val Glu Gly Ser Cys Cys Pro Met Cys
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 Pro Glu Met Tyr Val Pro Glu Pro Thr Asn Val Pro Ile Glu Lys Lys
 865 870 875 880
 Asn His Arg Gly Glu Ile Asp Leu Glu Val Pro Met Trp Pro Thr Pro
 885 890 895
 Ser Glu Asn Asp Ile Ile His Leu Pro Arg Asp Met Gly His Leu Gln
 900 905 910
 Val Asp Tyr Arg Asp Asn Asn Arg Leu His Pro Gly Glu Asp Ser Ser
 915 920 925
 Leu Asp Ser Ile Val Ser Val Val Val Pro Ile Ile Ile Cys Leu Ser
 930 935 940
 Ile Ile Ile Ala Phe Leu Leu Ile Asn Gln Lys Lys Gln Trp Val Pro
 945 950 955 960
 Leu Leu Cys Trp Tyr Arg Thr Pro Thr Lys Pro Ser Ser Leu Asn Asn
 965 970 975
 Gln Leu Val Ser Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp
 980 985 990
 Gly Pro Gln Arg Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser
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 Tyr Gln Thr Val
 1025

<210> 15
 <211> 2276
 <212> DNA
 <213> Homo sapiens

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 phosphatase catalytic subunit, calcineurin A alpha
 (PPP3CA) cDNA

<220>
 <221> CDS
 <222> (148)..(1713)
 <223> PPP3CA

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<210> 16

<211> 521

<212> PRT

<213> Homo sapiens

<220>

<223> human calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA)

<400> 16

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```

```

Val Val Lys Ala Val Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys
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```

```

Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
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```

```

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
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```

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 65 70 75 80
 Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
 85 90 95
 Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
 100 105 110
 Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
 115 120 125
 Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
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 Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
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 180 185 190
 Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
 195 200 205
 Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
 210 215 220
 Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
 225 230 235 240
 Asn Glu Lys Thr Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys
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 Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn
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 Asn Leu Leu Ser Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr
 275 280 285
 Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr
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 Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys
 325 330 335
 Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp
 340 345 350
 Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val
 355 360 365
 Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
 370 375 380

Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile
 385 390 395 400
 Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu
 405 410 415
 Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu
 420 425 430
 Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Thr
 435 440 445
 Val Glu Ala Ile Glu Ala Asp Glu Ala Ile Lys Gly Phe Ser Pro Gln
 450 455 460
 His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
 465 470 475 480
 Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
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 Asn Gly Ser Asn Ser Ser Asn Ile Gln
 515 520

<210> 17
 <211> 2194
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse calmodulin-dependent phosphoprotein
 phosphatase catalytic subunit, calcineurin A alpha
 (PPP3CA) cDNA

<220>
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 <222> (76)..(1641)
 <223> CTGF

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<210> 18

<211> 521

<212> PRT

<213> Mus musculus

<220>

<223> mouse calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA)

<400> 18

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Met Ser Glu Pro Lys Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg
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Val Val Lys Ala Val Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys
      20                      25                      30

Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
      35                      40                      45

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
      50                      55                      60

Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
      65                      70                      75                      80

Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
      85                      90                      95

Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
      100                      105                      110

Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
      115                      120                      125

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
      130                      135                      140

```

Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
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Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
165 170 175
Ala Cys Met Asp Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn
180 185 190
Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
195 200 205
Leu Asp Asp Ile Arg Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr
210 215 220
Gly Pro Met Cys Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly
225 230 235 240
Asn Glu Lys Thr Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys
245 250 255
Ser Tyr Phe Tyr Ser Tyr Pro Ala Val Cys Asp Phe Leu Gln His Asn
260 265 270
Asn Leu Leu Ser Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr
275 280 285
Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr
290 295 300
Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala
305 310 315 320
Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys
325 330 335
Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp
340 345 350
Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val
355 360 365
Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
370 375 380
Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile
385 390 395 400
Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu
405 410 415
Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu
420 425 430
Pro Ser Gly Val Leu Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Thr
435 440 445
Val Glu Ala Ile Glu Ala Asp Glu Ala Ile Lys Gly Phe Ser Pro Gln
450 455 460

His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn
 465 470 475 480

Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu
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Asn Ser Ile Asn Lys Ala Leu Ala Ser Glu Thr Asn Gly Thr Asp Ser
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Asn Gly Ser Asn Ser Ser Asn Ile Gln
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<210> 19
 <211> 2360
 <212> DNA
 <213> Rattus norvegicus

<220>
 <223> rat calmodulin-dependent phosphoprotein
 phosphatase catalytic subunit, calcineurin A alpha
 (PPP3CA) cDNA

<220>
 <221> CDS
 <222> (271)..(1806)
 <223> PPP3CA

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 gtcgctgtcc cccctcccg gtgactggag atgtccgagc ccaaggcgat tgatcccaag 300
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 ctgtatttgt gggccttgaa aattctttac cccaaaacac tgtttttact tcgtggaaac 720
 catgaatgta ggcacctaac agagtatttc acgttttaac aagaatgtaa aataaagtat 780
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```

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<210> 20

<211> 511

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat calmodulin-dependent phosphoprotein
phosphatase catalytic subunit, calcineurin A alpha
(PPP3CA)

<400> 20

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Met Ser Glu Pro Lys Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg
  1                      5                      10                      15

```

```

Val Val Lys Ala Val Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys
          20                      25                      30

```

```

Glu Val Phe Asp Asn Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala
          35                      40                      45

```

```

His Leu Met Lys Glu Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile
          50                      55                      60

```

```

Ile Thr Glu Gly Ala Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp
          65                      70                      75                      80

```

```

Ile Asp Ala Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe
          85                      90                      95

```

```

Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg
          100                      105                      110

```

```

Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu
          115                      120                      125

```

```

Cys Val Leu Tyr Leu Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu
          130                      135                      140

```

```

Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe
          145                      150                      155                      160

```

```

Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp
          165                      170                      175

```

```

Ala Cys Met Asp Ala Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn
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Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr
          195                      200                      205

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29

<210> 21
 <211> 3984
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human protein tyrosine phosphatase, non-receptor
 type 3 (PTPN3a) cDNA

<220>
 <221> CDS
 <222> (24) .. (2765)
 <223> PTPN3a

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<210> 22

<211> 913

<212> PRT

<213> Homo sapiens

<220>

<223> human protein tyrosine phosphatase, non-receptor
type 3 (PTPN3a)

<400> 22

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Met Thr Ser Arg Leu Arg Ala Leu Gly Gly Arg Ile Asn Asn Ile Arg
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```

```

Thr Ser Glu Leu Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser
          20             25             30

```

```

Ile His Phe Leu Asp Gly Val Val Gln Thr Phe Lys Val Thr Lys Gln
          35             40             45

```

```

Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
          50             55             60

```

```

Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
          65             70             75             80

```

```

Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
          85             90             95

```

```

Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
          100            105            110

```

```

Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
          115            120            125

```

```

Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
          130            135            140

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Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly Asp
 145 150 155 160
 Tyr Asn Ser Ser Ile His His Pro Gly Tyr Leu Ser Asp Ser His Phe
 165 170 175
 Ile Pro Asp Gln Asn Glu Asp Phe Leu Thr Lys Val Glu Ser Leu His
 180 185 190
 Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
 195 200 205
 Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Ser Gly
 210 215 220
 Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
 225 230 235 240
 Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
 245 250 255
 Asn Ile Leu Lys Ile Ser Phe Lys Arg Lys Lys Phe Phe Ile His Gln
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 Arg Gln Lys Gln Ala Glu Ser Arg Glu His Ile Val Ala Phe Asn Met
 275 280 285
 Leu Asn Tyr Arg Ser Cys Lys Asn Leu Trp Lys Ser Cys Val Glu His
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 His Thr Phe Phe Gln Ala Lys Lys Leu Leu Pro Gln Glu Lys Asn Val
 305 310 315 320
 Leu Ser Gln Tyr Trp Thr Met Gly Ser Arg Asn Thr Lys Lys Ser Val
 325 330 335
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 Ala Met Arg Arg Ser Leu Ser Val Glu His Leu Glu Thr Lys Ser Leu
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 Pro Ser Arg Ser Pro Pro Ile Thr Pro Asn Trp Arg Ser Pro Arg Leu
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 385 390 395 400
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 405 410 415
 Lys Gly Ser Leu Ala Pro Gln Asp Ser Asp Ser Glu Val Ser Gln Asn
 420 425 430
 Arg Ser Pro His Gln Glu Ser Leu Ser Glu Asn Asn Pro Ala Gln Ser
 435 440 445
 Tyr Leu Thr Gln Lys Ser Ser Ser Ser Val Ser Pro Ser Ser Asn Ala
 450 455 460

Pro Gly Ser Cys Ser Pro Asp Gly Val Asp Gln Gln Leu Leu Asp Asp
 465 470 475 480
 Phe His Arg Val Thr Lys Gly Gly Ser Thr Glu Asp Ala Ser Gln Tyr
 485 490 495
 Tyr Cys Asp Lys Asn Asp Asn Gly Asp Ser Tyr Leu Val Leu Ile Arg
 500 505 510
 Ile Thr Pro Asp Glu Asp Gly Lys Phe Gly Phe Asn Leu Lys Gly Gly
 515 520 525
 Val Asp Gln Lys Met Pro Leu Val Val Ser Arg Ile Asn Pro Glu Ser
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 565 570 575
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 595 600 605
 Asp Glu Leu Asn Gln Leu Phe Pro Glu Ala Ile Phe Pro Met Cys Pro
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 690 695 700
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 740 745 750
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 755 760 765
 Gly Phe His Ile Gln Cys Gln Ser Glu Asp Cys Thr Ile Ala Tyr Val
 770 775 780

Ser Arg Glu Met Leu Val Thr Asn Thr Gln Thr Gly Glu Glu His Thr
 785 790 795 800
 Val Thr His Leu Gln Tyr Val Ala Trp Pro Asp His Gly Ile Pro Asp
 805 810 815
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 835 840 845
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 850 855 860
 Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met Arg Asp Gln
 865 870 875 880
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 885 890 895
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<210> 23
 <211> 3087
 <212> DNA
 <213> Mus musculus

<220>
 <223> mouse protein tyrosine phosphatase, non-receptor
 type 3 (PTPN3) cDNA

<220>
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 <222> (1)..(3087)
 <223> PTPN3

<400> 23
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<210> 24

<211> 1028

<212> PRT

<213> Mus musculus

<220>

<223> mouse protein tyrosine phosphatase, non-receptor
type 3 (PTPN3)

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35 40 45

Leu Ala Arg Lys Tyr Ile Pro Asp Ser Ser Asp Ile Phe Ile Glu Lys
50 55 60

Gly Met Val Glu Val Val Gly Tyr Ser Ala Ala Val Met Thr Ser Arg
65 70 75 80

Leu Arg Ala Leu Gly Gly Arg Ile Asn Asn Thr Arg Thr Ser Glu Leu
 85 90 95

Pro Lys Glu Lys Thr Arg Ser Glu Val Ile Cys Ser Ile Arg Phe Leu
 100 105 110

Asp Gly Leu Val Gln Thr Phe Lys Val Asn Lys Gln Asp Leu Gly Gln
 115 120 125

Ser Leu Leu Asp Met Ala Tyr Gly His Leu Gly Val Thr Glu Lys Glu
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Tyr Phe Gly Leu Gln His Gly Asp Asp Pro Val Asp Ser Pro Arg Trp
 145 150 155 160

Leu Glu Ala Ser Lys Pro Leu Arg Lys Gln Leu Lys Gly Glu Tyr Ala
 165 170 175

Leu Ala Ser Leu Gly Arg Trp Val Tyr Gly Lys Leu Ser Ser Pro Tyr
 180 185 190

Gly Gly Leu Lys Val Ala Gly Lys Pro Asn Leu Phe Leu Lys Asn Val
 195 200 205

Val Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Tyr Phe Ile
 210 215 220

Pro Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe
 225 230 235 240

Leu Gln Leu Lys Met Asp Val Cys Glu Gly Arg Leu Thr Cys Pro Leu
 245 250 255

Asn Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly
 260 265 270

Asp Phe Asn Ser Ser Ile His His Pro Gly Tyr Leu Ala Asp Ser Gln
 275 280 285

Phe Ile Pro Asp Gln Asn Asp Asp Phe Leu Ser Lys Val Glu Ser Leu
 290 295 300

His Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr
 305 310 315 320

Ile Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Gly
 325 330 335

Gly Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala
 340 345 350

Gly Ile Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp
 355 360 365

Lys Lys Phe Phe Ile His Gln Arg Gln Lys Gln Glu Glu Lys Ile Val
 370 375 380

Ala Val Arg Ser Ser Asp Pro Val Ala Ile Ser Ala Glu Ser Arg Glu
 385 390 395 400

His Ile Val Ala Phe Asn Met Leu Asn Tyr Arg Ser Cys Lys Asn Leu
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 Trp Lys Ser Cys Val Glu His His Ser Phe Phe Gln Ala Lys Lys Leu
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 Leu Pro Gln Glu Lys Asn Val Leu Ser Gln Tyr Trp Thr Leu Gly Ser
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 Gly Gly Met Val Trp Asn Pro Val Met Arg Arg Ser Leu Ser Val Glu
 465 470 475 480
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 485 490 495
 Asn Trp Arg Ser Pro Arg Leu Arg His Glu Ile Arg Lys Pro Arg His
 500 505 510
 Ser Ser Ala Asp Asn Leu Ala Asn Glu Met Thr Tyr Ile Thr Glu Thr
 515 520 525
 Glu Asp Val Phe Tyr Thr Tyr Lys Gly Pro Leu Ser Pro Lys Asp Ser
 530 535 540
 Asp Ser Glu Val Ser Gln Asn His Ser Pro His Arg Glu Ser Leu Ser
 545 550 555 560
 Glu Asn Asn Pro Ala Gln Ser Cys Leu Thr Gln Lys Ser Ser Ser Ser
 565 570 575
 Val Ser Pro Ser Ser Asn Ala Pro Gly Ser Cys Ser Pro Asp Gly Val
 580 585 590
 Asp Gln Arg Phe Leu Glu Asp Tyr His Lys Val Thr Lys Gly Gly Phe
 595 600 605
 Val Glu Asp Ala Ser Gln Tyr Tyr Cys Asp Lys Ser Asp Asp Gly Asp
 610 615 620
 Gly Tyr Leu Val Leu Ile Arg Ile Thr Pro Asp Glu Glu Gly Arg Phe
 625 630 635 640
 Gly Phe Asn Leu Lys Ala Asp Thr Cys Met Pro Lys Leu Asn Glu Gly
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 Asp Gln Ile Val Leu Ile Asn Gly Arg Asp Ile Ser Glu His Thr His
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 Asp Gln Val Val Met Phe Ile Lys Ala Ser Arg Glu Ser His Ser Arg
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 Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
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 Asn Met Glu Met Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
 820 825 830
 Gln Gly Pro Leu Pro Asn Thr Cys Ala Gln Phe Trp Gln Val Val Trp
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 Asp Gln Lys Leu Ser Leu Val Val Met Leu Thr Thr Leu Thr Glu Arg
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 Val Pro Asp Asp Ser Ser Asp Phe Leu Glu Phe Val Lys Tyr Val Arg
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 980 985 990
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 <213> Homo sapiens

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 type 3 (PTPN3b) splice variant cDNA

<220>
 <221> CDS
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 <223> PTPN3b splice variant

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 <212> PRT
 <213> Homo sapiens

<220>
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 type 3 (PTPN3b) splice variant

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 35 40 45
 Asp Thr Gly Gln Val Leu Leu Asp Met Val His Asn His Leu Gly Val
 50 55 60
 Thr Glu Lys Glu Tyr Phe Gly Leu Gln His Asp Asp Asp Ser Val Asp
 65 70 75 80
 Ser Pro Arg Trp Leu Glu Ala Ser Lys Pro Ile Arg Lys Gln Leu Lys
 85 90 95
 Gly Gly Phe Pro Cys Thr Leu His Phe Arg Val Arg Phe Phe Ile Pro
 100 105 110
 Asp Pro Asn Thr Leu Gln Gln Glu Gln Thr Arg His Leu Tyr Phe Leu
 115 120 125
 Gln Leu Lys Met Asp Ile Cys Glu Gly Arg Leu Thr Cys Pro Leu Asn
 130 135 140
 Ser Ala Val Val Leu Ala Ser Tyr Ala Val Gln Ser His Phe Gly Asp
 145 150 155 160
 Tyr Asn Ser Ser Ile His His Pro Gly Tyr Leu Ser Asp Ser His Phe
 165 170 175
 Ile Pro Asp Gln Asn Glu Asp Phe Leu Thr Lys Val Glu Ser Leu His
 180 185 190
 Glu Gln His Ser Gly Leu Lys Gln Ser Glu Ala Glu Ser Cys Tyr Ile
 195 200 205
 Asn Ile Ala Arg Thr Leu Asp Phe Tyr Gly Val Glu Leu His Ser Gly
 210 215 220
 Arg Asp Leu His Asn Leu Asp Leu Met Ile Gly Ile Ala Ser Ala Gly
 225 230 235 240
 Val Ala Val Tyr Arg Lys Tyr Ile Cys Thr Ser Phe Tyr Pro Trp Val
 245 250 255
 Asn Ile Leu Lys Ile Ser Phe Lys Arg Lys Lys Phe Phe Ile His Gln
 260 265 270

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gln | Lys | Gln | Ala | Glu | Ser | Arg | Glu | His | Ile | Val | Ala | Phe | Asn | Met | 275 | 280 | 285 | |
| Leu | Asn | Tyr | Arg | Ser | Cys | Lys | Asn | Leu | Trp | Lys | Ser | Cys | Val | Glu | His | 290 | 295 | 300 | |
| His | Thr | Phe | Phe | Gln | Ala | Lys | Lys | Leu | Leu | Pro | Gln | Glu | Lys | Asn | Val | 305 | 310 | 315 | 320 |
| Leu | Ser | Gln | Tyr | Trp | Thr | Met | Gly | Ser | Arg | Asn | Thr | Lys | Lys | Arg | Ser | 325 | 330 | 335 | |
| Pro | Arg | Leu | Arg | His | Glu | Ile | Arg | Lys | Pro | Arg | His | Ser | Ser | Ala | Asp | 340 | 345 | 350 | |
| Asn | Leu | Ala | Asn | Glu | Met | Thr | Tyr | Ile | Thr | Glu | Thr | Glu | Asp | Val | Phe | 355 | 360 | 365 | |
| Tyr | Thr | Tyr | Lys | Gly | Ser | Leu | Ala | Pro | Gln | Asp | Ser | Asp | Ser | Glu | Val | 370 | 375 | 380 | |
| Ser | Gln | Asn | Arg | Ser | Pro | His | Gln | Glu | Ser | Leu | Ser | Glu | Asn | Asn | Pro | 385 | 390 | 395 | 400 |
| Ala | Gln | Ser | Tyr | Leu | Thr | Gln | Lys | Ser | Ser | Ser | Ser | Val | Ser | Pro | Ser | 405 | 410 | 415 | |
| Ser | Asn | Ala | Pro | Gly | Ser | Cys | Ser | Pro | Asp | Gly | Val | Asp | Gln | Gln | Leu | 420 | 425 | 430 | |
| Leu | Asp | Asp | Phe | His | Arg | Val | Thr | Lys | Gly | Gly | Ser | Thr | Glu | Asp | Ala | 435 | 440 | 445 | |
| Ser | Gln | Tyr | Tyr | Cys | Asp | Lys | Asn | Asp | Asn | Gly | Asp | Ser | Tyr | Leu | Val | 450 | 455 | 460 | |
| Leu | Ile | Arg | Ile | Thr | Pro | Asp | Glu | Asp | Gly | Lys | Phe | Gly | Phe | Asn | Leu | 465 | 470 | 475 | 480 |
| Lys | Gly | Gly | Val | Asp | Gln | Lys | Met | Pro | Leu | Val | Val | Ser | Arg | Ile | Asn | 485 | 490 | 495 | |
| Pro | Glu | Ser | Pro | Ala | Asp | Thr | Cys | Ile | Pro | Lys | Leu | Asn | Glu | Gly | Asp | 500 | 505 | 510 | |
| Gln | Ile | Val | Leu | Ile | Asn | Gly | Arg | Asp | Ile | Ser | Glu | His | Thr | His | Asp | 515 | 520 | 525 | |
| Gln | Val | Val | Met | Phe | Ile | Lys | Ala | Ser | Arg | Glu | Ser | His | Ser | Arg | Glu | 530 | 535 | 540 | |
| Leu | Ala | Leu | Val | Ile | Arg | Arg | Arg | Ala | Val | Arg | Ser | Phe | Ala | Asp | Phe | 545 | 550 | 555 | 560 |
| Lys | Ser | Glu | Asp | Glu | Leu | Asn | Gln | Leu | Phe | Pro | Glu | Ala | Ile | Phe | Pro | 565 | 570 | 575 | |
| Met | Cys | Pro | Glu | Gly | Gly | Asp | Thr | Leu | Glu | Gly | Ser | Met | Ala | Gln | Leu | 580 | 585 | 590 | |

Lys Lys Gly Leu Glu Ser Gly Thr Val Leu Ile Gln Phe Glu Gln Leu
 595 600 605
 Tyr Arg Lys Lys Pro Gly Leu Ala Ile Thr Phe Ala Lys Leu Pro Gln
 610 615 620
 Asn Leu Asp Lys Asn Arg Tyr Lys Asp Val Leu Pro Tyr Asp Thr Thr
 625 630 635 640
 Arg Val Leu Leu Gln Gly Asn Glu Asp Tyr Ile Asn Ala Ser Tyr Val
 645 650 655
 Asn Met Glu Ile Pro Ala Ala Asn Leu Val Asn Lys Tyr Ile Ala Thr
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 Thr Glu Arg Asn Leu Pro Ile Tyr Pro Leu Asp Ile Val Arg Lys Met
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 Arg Asp Gln Arg Ala Met Met Val Gln Thr Ser Ser Gln Tyr Lys Phe
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 (tyrosine/serine), catalytic domain (DUSP3) cDNA

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 <222> (29)..(586)
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 gaaacacact gtaccctgct ccagcatca caaggcactt gtctacaagt gtgtcccaac 720
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<210> 28
 <211> 185
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<220>
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 (tyrosine/serine), catalytic domain (DUSP3)

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 Met Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
 1 5 10 15
 Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
 20 25 30
 Val Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
 35 40 45
 Pro Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
 50 55 60
 Gly Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp
 65 70 75 80
 Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
 85 90 95
 Asn Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala
 100 105 110
 Leu Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
 115 120 125

Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
 130 135 140

Met Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile
 145 150 155 160

Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
 165 170 175

Leu Ala Lys Glu Gly Lys Leu Lys Pro
 180 185

<210> 29

<211> 1196

<212> DNA

<213> Mus musculus

<220>

<223> mouse dual specificity phosphatase
 (tyrosine/serine), catalytic domain (DUSP3) cDNA

<220>

<221> CDS

<222> (64)..(621)

<223> DUSP3

<400> 29

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agcggctgct acagcctgcc gagccagccc tgcaacgagg tcgtcccagag ggtctacgtg 180
ggcaacgcgt ctgtgggtca ggacatcacc cagctgcaga aactgggcat caccacgctc 240
ctgaatgctg ccgagggcag gtccttcatt cagctcaaca ccagtgctag cttctacgag 300
gattctggca tcacctactt gggcatcaag gccaatgata cgcaggagtt caacctcagt 360
gcttactttg aaagggccac agatttcatt gaccaggcgc tggcccataa aaatggccgg 420
gtgcttgctc attgccgcga gggctacagc cgctcccca cgtagttat cgcctacctc 480
atgatgcggc agaagatgga cgtcaagtct gctctgagta ctgtgaggca gaatcgtgag 540
atcgggccca acgatggctt cctggcccaa ctctgccagc tcaatgacag actagccaag 600
gagggaagg tgaaactcta gggtgccac agcctctttt gcagagggtc gactgggagg 660
gccctggcag ccatgtttag gaaacacagt ataccactc cctgcaccac cagacacgtg 720
cccacatctg tcccactctg gtccctgggg gccactccac ccttagggag cacatgaaga 780
agctccctaa gaagttctgc tccttagcca tcctttcctg taatttatgt ctctccctga 840
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ggagggctat caggggtgat ggcccgggac acgggcactc ttcattgacct ctccccacc 960
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cgaatgacat taagttctga agcagagtgg agatagatta gtgactagat ttccaaaaag 1140
aaggaaaaaa aaggctgcat tttaaaatta tttccttaga attaaagata ctacat 1196

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<210> 30

<211> 185

<212> PRT

<213> Mus musculus

<220>

<223> mouse dual specificity phosphatase
 (tyrosine/serine), catalytic domain (DUSP3)

<400> 30
Met Ser Ser Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu
1 5 10 15
Ser Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu
20 25 30
Val Val Pro Arg Val Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile
35 40 45
Thr Gln Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu
50 55 60
Gly Arg Ser Phe Met His Val Asn Thr Ser Ala Ser Phe Tyr Glu Asp
65 70 75 80
Ser Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe
85 90 95
Asn Leu Ser Ala Tyr Phe Glu Arg Ala Thr Asp Phe Ile Asp Gln Ala
100 105 110
Leu Ala His Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr
115 120 125
Ser Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys
130 135 140
Met Asp Val Lys Ser Ala Leu Ser Thr Val Arg Gln Asn Arg Glu Ile
145 150 155 160
Gly Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg
165 170 175
Leu Ala Lys Glu Gly Lys Val Lys Leu
180 185

<210> 31
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<223> human regulator of G-protein signaling 10 (RGS10)
cDNA

<220>
<221> CDS
<222> (133)..(636)
<223> RGS10

<400> 31
taccgagctc ggatccacta gtaacggccg ccagtgtgct ggaattcgcc cttactcact 60
atagggctcg agcggccgcc cgggcaggtg gattgttggt ctgctggaa cttctcaggt 120
ggacaccaga gcatggaaca catccacgac agcgatggca gttccagcag cagccaccag 180
agcctcaaga gcacagccaa atgggcggca tccctggaga atctgctgga agaccagaaa 240
ggcgtgaaaa gatttaggga atttttaaaa aaggaattca gtgaagaaaa tgttttgttt 300
tggctagcat gtgaagattt taagaaaatg caagataaga cgcagatgca ggaaaaggca 360
aaggagatct acatgacctt tctgtccagc aaggcctcat cacagggtcaa cgtggagggg 420
cagtctcggc tcaacgagaa gatcctggaa gaaccgcacc ctctgatgtt ccagaaaactc 480

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caggaccaga tctttaatct catgaagtac gacagctaca gccgctttct taagtctgac 540
ttgttttttaa aacacaagcg aaccgaggaa gaggaagaag atttgctga tgctcaaact 600
gcagctaaaa gagcttccag aatttataac acatgagccc ccaaaaagcc gggactggca 660
gctttaagaa gcaaaggaat ttcctctcag gacgtgccgg gtttatcatt gctttgttat 720
ttgtaaggac tgaatgtac aaaacccttc aat 753

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<210> 32
<211> 167
<212> PRT
<213> Homo sapiens

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<220>
<223> human regulator of G-protein signaling 10 (RGS10)

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<400> 32
Met Glu His Ile His Asp Ser Asp Gly Ser Ser Ser Ser Ser His Gln
  1              5              10              15

Ser Leu Lys Ser Thr Ala Lys Trp Ala Ala Ser Leu Glu Asn Leu Leu
      20              25              30

Glu Asp Pro Glu Gly Val Lys Arg Phe Arg Glu Phe Leu Lys Lys Glu
      35              40              45

Phe Ser Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys
      50              55              60

Lys Met Gln Asp Lys Thr Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr
      65              70              75              80

Met Thr Phe Leu Ser Ser Lys Ala Ser Ser Gln Val Asn Val Glu Gly
      85              90              95

Gln Ser Arg Leu Asn Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met
      100             105             110

Phe Gln Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser
      115             120             125

Tyr Ser Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys His Lys Arg Thr
      130             135             140

Glu Glu Glu Glu Glu Asp Leu Pro Asp Ala Gln Thr Ala Ala Lys Arg
      145             150             155             160

Ala Ser Arg Ile Tyr Asn Thr
      165

```

```

<210> 33
<211> 877
<212> DNA
<213> Mus musculus

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<220>
<223> mouse regulator of G-protein signaling 10 (RGS10)
      cDNA

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<220>
 <221> CDS
 <222> (60)..(605)
 <223> RGS10

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<400> 33
gctcttcggg cttagccgcc gcgctgccc gctgctccgt cctctggacg cccgcggcga 60
tggtcaccgc cgccgtgagc cgactgagca ggaagcggcc gccgtctgat atccatgacg 120
gagatgggag ctcaagcagc ggccaccaga gccttaagag cacagccaag tgggcaccc 180
ccctggagaa tcttctggaa gaccagaag gggtgcagag attcaggag tttctgaaga 240
aggaattcag cgaagagaat gtcttgtttt ggctagcgtg tgaagatttc aagaaaacgg 300
aggacaggaa gcagatgcag gaaaaggcca aggagatcta catgaccttc ctgtccaata 360
aggcctcttc acaagtcaac gtggaggggc agtctcggct cactgaaaag attctggaag 420
agccacaccc tctgatgttc caaaagctcc aggaccagat cttcaatctc atgaagtatg 480
acagctacag ccgcttcttg aagtctgact tgtttctgaa acccaagcga actgaggaag 540
aggaagaaga gcccccgat gctcagaccg cagctaagcg agcctccaga atttacaaca 600
cataagctga gcccttcacc ccagcgaagg agagggatgg actcttagga ctgtacaggc 660
tgtcatttct ttgttggttg tgaggactgg agtggtgctag acctccctc tggatatgtg 720
tattttatta actgaacagc aacctctgca tgatgctaata cttccattaa aaacaaaagt 780
agctttaaag tgtcagttca caaaaacaca tgagattctg ccaataactgg aactcagcc 840
tttcaatcct gattaaagtg ttcgtgaagc tacaagc 877

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<210> 34
 <211> 181
 <212> PRT
 <213> Mus musculus

<220>
 <223> mouse regulator of G-protein signaling 10 (RGS10)

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<400> 34
Met Phe Thr Arg Ala Val Ser Arg Leu Ser Arg Lys Arg Pro Pro Ser
  1             5             10             15

Asp Ile His Asp Gly Asp Gly Ser Ser Ser Gly His Gln Ser Leu
      20             25             30

Lys Ser Thr Ala Lys Trp Ala Ser Ser Leu Glu Asn Leu Leu Glu Asp
      35             40             45

Pro Glu Gly Val Gln Arg Phe Arg Glu Phe Leu Lys Lys Glu Phe Ser
      50             55             60

Glu Glu Asn Val Leu Phe Trp Leu Ala Cys Glu Asp Phe Lys Lys Thr
      65             70             75             80

Glu Asp Arg Lys Gln Met Gln Glu Lys Ala Lys Glu Ile Tyr Met Thr
      85             90             95

Phe Leu Ser Asn Lys Ala Ser Ser Gln Val Asn Val Glu Gly Gln Ser
      100            105            110

Arg Leu Thr Glu Lys Ile Leu Glu Glu Pro His Pro Leu Met Phe Gln
      115            120            125

Lys Leu Gln Asp Gln Ile Phe Asn Leu Met Lys Tyr Asp Ser Tyr Ser
      130            135            140

Arg Phe Leu Lys Ser Asp Leu Phe Leu Lys Pro Lys Arg Thr Glu Glu
      145            150            155            160

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Glu Glu Glu Glu Pro Pro Asp Ala Gln Thr Ala Ala Lys Arg Ala Ser
165 170 175

Arg Ile Tyr Asn Thr
180

<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hexahistidine
(His) affinity tag

<400> 35
His His His His His His
1 5

<210> 36
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:poly-Gly
flexible linker

<220>
<221> MOD_RES
<222> (6)..(200)
<223> Gly residues from position 6 to 200 may be present
or absent

<400> 36
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
35 40 45
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
65 70 75 80
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
85 90 95
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
100 105 110
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
115 120 125

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190

Gly Gly Gly Gly Gly Gly Gly Gly
 195 200